THE CLAIMS

Presented below are the claims pursuant to 37 C.F.R. 1.121. Claim 1 is amended herein. Claims 25-27 are new.

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1. (currently amended) A method of identifying a compound that modulates intermolecular interactions between a target protein and a modifier comprising the steps of

a) reviewing a three dimensional structure of said target protein;

b) identifying a flexible site within the structure of the target protein which comprises a functionally critical site;

~~a)~~ c) identifying a cavity within the flexible site on said target protein, that is about 15-20 Ångstroms proximal to, but at a distinct location from, the functionally critical site of said target protein, which cavity is involved in intermolecular interactions with said modifier;

~~b)~~ d) calculating dimensions of said cavity and mapping chemical and/or electrostatic properties of said cavity;

~~c)~~ e)identifying compounds that contain functional groups that can be accommodated by said cavity; and

~~d)~~ f) testing said compounds in an in vitro assay to detect a compound which binds to the proximal site and allosterically modulates intermolecular interactions between said target protein and said modifier at the functionally critical site.

2. (withdrawn from consideration) A pharmaceutical composition comprising:

a) a pharmaceutically acceptable carrier of diluent; and

b) a therapeutically effective amount of a compound having a structure selected from the group consisting of Formulae I-XIX.

3. (withdrawn from consideration) A method of treating an individual suffering from an inflammatory condition comprising the step of administering to said individual

19. (withdrawn from consideration) The method of claim 18, wherein the modifier is a protein selected from the group consisting of a membrane-bound protein, a cytosolic protein, a nuclear protein, an enzyme substrate, a cytokine, a lymphokine, a chemokine, an adhesion molecule, a growth factor, or a receptor thereof.

20. (withdrawn from consideration) The method of claim 18, wherein the modifier is a member of the TNF receptor superfamily.

21. (withdrawn from consideration) The method of claim 18, wherein the modifier is selected from the group consisting of TNF receptor, fas, CD40, gp120, fas ligand, TNF-□, ß-lactam, c-erbB2, growth hormone receptor, growth hormone, insulin receptor, insulin, IL-1 receptor, IL-1, IL-2 receptor, IL-2, epidermal growth factor receptor (EGFR), MHC/antigen/TCR complex, and epidermal growth factor.

22. (withdrawn from consideration) The method of claim 21, wherein the modifier is TNF-α.

23. (withdrawn from consideration) The method of claim 19, wherein the modifier is ß-lactam.

24. (withdrawn from consideration) The method of claim 19, wherein the modifier is the MHC/antigen/TCR complex.

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25. (new) The method of claim 1, wherein identifying a flexible site within the structure of a target protein in step b) comprises identifying thermal β-factors, using calorimetric values from thermodynamic studies, or using algorithms.

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26. (new) A method of identifying a compound that modulates intermolecular interactions between a target protein and a modifier comprising the steps of

a) reviewing a three dimensional structure of said target protein for which a three dimensional structure is available;

b) identifying a flexible site within the structure of the target protein which comprises a functionally critical site;

c) identifying a cavity within the flexible site on said target protein that is about 15-20 Ångstroms proximal to, but at a distinct location from, a functionally critical site of said target protein, which cavity is involved in intermolecular interactions with said modifier;

d) calculating dimensions of said cavity and mapping chemical and/or electrostatic properties of said cavity;

e) identifying compounds that contain functional groups that can be accommodated by said cavity; and

f) testing said compounds in an in vitro assay to detect a compound which binds to the proximal site and allosterically modulates intermolecular interactions between said target protein and said modifier at the functionally critical site.

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27. The method of claim 26, wherein identifying a flexible site within the structure of a target protein in step b) comprises identifying thermal β-factors, using calorimetric values from thermodynamic studies, or using algorithms.